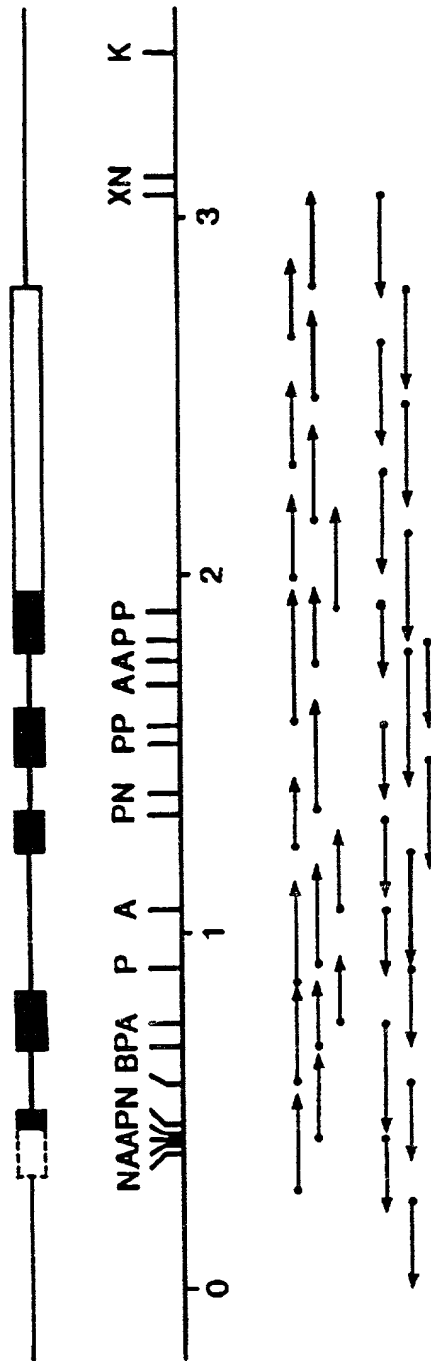


1 / 16

FIG.1



2 / 16

**FIG. 2A**

[illegible]

3 / 16

## FIG. 2B

110 Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly  
 CTG CAG CTG GAC GAC GAC TTT GCC ACC ACC ATC TGG CAG CAG ATG GAA GAA CTT CTT GAC CCT  
 GAC GTC GAC CTG CAG CGG CTG AAA CGG TGG TAG ACC GTC GTC TAC CTT GAC CCT

120

130 Met Ala Pro Ala Gln Leu Gln Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln  
 ATG GCC CCT GCC CAG CTG CAG CCC ACC CAG GGT GCC ATG CCG GCC TTC GCC TCT GCT TTC CAG  
 TAC CGG GGA CGG GAC GTC GTC GCG TGG CTC CCA CGG TAC GGC CGG AAG CGG AGA CGA AAG GTC

140

150 Arg Arg Ala Gly Gln Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr  
 CGC CGG GCA GGA GGG GTC GTC CTG GTT GCC TCC CAT CTG CAG AGC TTC CTG GAG GTG TCG TAC  
 GCG GCC CGT CCT CCC CAG GAC CAA CGG AGG GTA GAC GTC TCG AAG GAC CTC CAC AGC ATG

160

170 Arg Val Leu Arg His Leu Ala Gln Pro OP  
 CGC GTT CTA CGC CAC CTT GCC CAG CCC TGA GCC AAG CCC TCC CCA TCC CAT GTA TTT ATC  
 CGC CAA GAT GCG GTG GAA CGG GTC GGC ACT

174

TCT ATT TAA TAT TTA TGT CTA TTT AAG CCT CAT ATT TAA AGA CAG GGA AGA GCA GAA CGG

AGC CCC AGG CCT CTG TGT CCT TCC CTG CAT TTC TGA GTT TCA TTC TCC TCG CTG TAG CAG  
StuI

TGA GAA AAA GCT CCT GTC CTC CCA TCC CCT GGA CTG GGA GGT AGA TAG GTA AAT ACC AAG

TAT TTA TTA CTA TGA CTG CTC CCC AGC CCT GGC TCT GCA ATG GGC ACT GGG ATG AGC CGC

TGT GAG CCC CTG GTC CTG AGG GTC CCC ACC TGG GAC CCT TGA GAG TAT CAG GTC TCC CAC

4 / 16

## FIG. 2C

GTG GGA GAC AAG AAA TCC CTG TTT AAT ATT TAA ACA GCA GTG TTC CCC ATC TGG GTC CTT  
GCA CCC CTC ACT CTG GCC TCA GCC GAC TGC ACA GCG GCC CCT GCA TCC CCT TGG CTG TGA  
GGC CCC TGG ACA AGC AGA GGT GGC CAG AGC TGG GAG GCA TGG CCC TGG GGT CCC ACG AAT  
TTG CTG GGG AAT CTC GTT TTT CTT AAG ACT TTT GGG ACA TGG TTT GAC TCC CGA ACA  
TCA CCG ACG TGT CTC CTG TTT TTC TGG GTG GCC TCG GGA CAC CTG CCC TGC CCC CAC GAG  
GGT CAG GAC TGT GAC TCT TTT TAG GGC CAG GCA GGT GCC TGG ACA TTT GCC TTG CTG GAC  
GGG GAC TGG GGA TGT GGG AGG AGG GAG CAG ACA GGA GGA ATC ATG TCA GGC CTG TGT GTG AAA  
GGA AGC TCC ACT GTC ACC CTC CAC CTC TTC ACC CCC CAC TCA CCA GTG TCC CCT CCA CTG  
TCA CAT TGT AAC TGA ACT TCA GGA TAA TAA AGT GTT TGC CTC CA

[f150-200 base poly A plus 25-30 bases plasmid DNA preceding a PvuII restriction site]-3'

5 / 16

```
GGGGACAGGCTTGAGAAATCCCAAAGGAGAGGGGCAAAGGACACTGCCCCCGCAAGTCTGCCAGAGCAGAG 70
AGGAGACCCCGACTCAGCTGCCACTTCCCCACAGGCTCGTGCCGCTTCCAGGCGTCTATCAGCGGCTCA 140
GCCTTTGTTCAGCTGTTCTGTTCAAACACTCTGGGGCCATTTCAGGCCCTGGGTGGGCAGCGGAGGAAGG 210
GAGTTTGAGGGGGCAAGGCGACGTCAAAGGAGGATCAGAGATTCCACAATTTCACAAAACTTTCGCAAA 280
CAGCTTTTGTTCCAACCCCGGAGCCTTGCAATTGTTGGACACCAAAATTTCGCATAAAATCCTGGGAAGTTATTAC 350
TAAGCCTTAGTCGTGGCCCCCAGGTAATTTCCTCCAGGCCCTCCATGGGGTTATGTATAAAGGGCCCCCTA 420
GAGCTGGGCCCCAAACAGCCCGGAGCCTGCAGCCCGCCAGCCCCACCCAGACCCATGGCTGGACCTGCCACC 490
GlnSerProMetLysLeuMeta
CAGAGCCCCCATGAAGCTGATGGGTGAGTGTCTTGGCCCCAGGATGGGAGAGCCCGCTGCCCTGGCATGGGA 560
GGGAGGCTGGTGTGACAGAGGGGCTGGGGATCCCGTTCTGGGAATGGGGATTAAAGGCACCCAGTGTCC 630
CCGAGAGGGCCTCAGGTGGTAGGGAACAGCATGTCTCCTGAGCCCCGCTCTGTCCCCCAGCCCCCTGCAGCTGC 700
LeuGlnLeuL
```

FIG. 3A

6 / 16

-10 -1 +1 10  
euLeuTrpHisSerAlaLeuTrpThrValGlnGluAlaThrProLeuGlyProAlaSerSerLeuProGlu 770  
TGCTGTGGCACAGTGCACTCTGGACAGTGCAGGAAGCCACCCCTGGGCCCTGCCAGCTCCTGCCCCA 30  
nSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLys 840  
GAGCTTCCTGCTCAAGTGCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAAG 35  
Leu 35  
CTGGTGAGTGAGGTGGTGAGAGGGCTGTGGAGGGGAAGCCCGGTGGGGAGAGCTAAGGGGGATGGAACTG 910  
CAGGGCCAACATCCTCTGGAAAGGACATGGGAGAAATATTAGAGCAGTGGAGCTGGGGAAGGCTGGGAAG 980  
GGACTTGGGGAGGAGGACCTTGTTGGGGACAGTGCTCGGGAGGGCTGGCTGGGATGGGAGTGGAGGCATC 1050  
ACATTCAGGAGAAAGGGCAAGGGCCCCCTGTGAGATCAGAGAGTGGGGGTGCAGGGCAGAGAGAACTGAA 1120  
CAGCCTGGCAGGACATGGAGGGAGGGGAAAGACCAGAGAGTCTGGGGAGGACCCGGGAAGAGCGCGACC 1190  
CGGCCACGGCGAGTCTCACTCAGCATCCTTCCATCCCCAGTGTGCCACCTACAAGCTGTGCCACCCCGAG 36 40  
CysAlaThrTyrLysLeuCysHisProGlu  
GluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaL 60  
GAGCTGGTGCTGCGACACTCTCTGGGCATCCCCCTGGGCTCCCCCTGAGCAGCTGCCCCAGCCAGGCC 50 1330

FIG. 3B

FIG. 3B

7 / 16

70 71  
euGlnLeu  
TGCAGCTGGTGAGTGTCAAGAAAGGATAAGGCTAATGAGGAGGGGGAAGGAGAGGAAACACCCATGGG 1400  
CTCCCCCATGTCTCCAGGTTCCAAAGCTGGGGGCTGACGTATCTCAGGCAGCACCCCTAACTCTTCCGC 1470  
72 80 90  
AlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnA  
TCTGTCTCACAGGCAGGCTGCTTGAGCCAACTCCATAGCGGCCTTTTCTCTACCCAGGGCTCCTGCAGG 1540  
100 110  
1aLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAl  
CCCTGGAAAGGATCTCCCCCGAGTTGGTCCCACCTTGGACACACTGCAGCTGGACGTGCGCCGACTTTGC 1610  
120  
aThrThrIleTrpGlnGln  
CACCACTCTGGCAGCAGGTGAGCCTTGTGGGCAGGGTGCCCAAGTCTGTGCTGGCATTTCTGGGCACC 1680  
121  
ACAGCCGGCCCTGTGTATGGGCCCTGTCCATGCTGTCTCAGCCCCCAGCATTTCTCATTTGTATAACGCC 1750  
MetGluGluLeuGlyMetAlaProAla  
CACTCAGAAGGCCCAACCACTGATCACAGCTTTCCCCCACAGATGGAAGAACTGGGAATGGCCCCCTGCC 1820  
130 140 150  
LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuV  
CTGCAGCCCAACCAGGTGCCATGCCGGCCTTCGCCCTCTGCTTTCCAGCGCCGGGCAGGAGGGGTCTCTGG 1890

FIG. 3C

8 / 16

160	170	174
alAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnProOP		
TTGCCCTCCCATCTGCAGAGCTTCCTGGAGGTGTCTGACCGGTTCTACGCCACCTTGCCCGAGCCCTGAGC		1960
CAAGCCCTCCCCATCCCATGTATTTATCTCTATTTAATAATTTATGTCTATTTAAGCCTCATATTTAAAGA		2030
CAGGGAAGAGCAGAACGGAGCCCGAGGCCCTCTGTGTCCCTTCCCTGCAATTTCTGAGTTTCAATTCCTCTGCC		2100
TGTAGCAGTGAGAAAAGCTCCTGTCTCCCTCCCATCCCTGGACTGGGAGGTAGATAGTAAATACCAAGTA		2170
TTTATTACTATGACTGCTCCCCAGCCCTGGCTCTGCAATGGGCACTGGGATGAGCCGCTGTGAGCCCCCTG		2240
GTCCCTGAGGGTCCCCACCTGGGACCCCTTGAGAGTATCAGGTCTCTCCACGCTGGGAGACAAGAAATCCCTGT		2310
TTAATAATTTAAACAGCAGTGTTCCCCATCTGGGTCTCTTGACCCCTCACTCTGGCCCTCAGCCGACTGCAC		2380
AGCGGCCCCTGCAATCCCTTGGCTGTGAGGCCCTTGACAAAGCAGAGGTGGCCAGAGCTGGGAGGCATGG		2450
CCCTGGGGTCCCACGAATTGCTGGGGAATCTCGTTTTTCTTCTTAAGACTTTTGGGACATGGTTTGACT		2520
CCCGAACATCACCGACGTGTCTCCTGTTTTTCTGGGTGGCCCTCGGGACACCTGCCCCCTGCCCCACGAGGG		2590

FIG. 3D

Sequence 236668



9 / 16

TCAGGACTGTGACTCTTTTAGGGCCAGGCAGGTGCCCTGGACATTTGCCCTTGCTGGATGGGGACTGGGGA 2660  
TGTGGGAGGAGCAGACAGGAGGAATCATGTCAGGCCCTGTGTGTGAAAGGAAGCTCCACTGTCAACCCTCC  
ACCTCTTCACCCCCACTACCAAGTGTCCCTCCACTGTCACATGTAACTGAACCTTCAGGATAATAAAG 2800  
TGTTTGCCCTCCAGTCACGTCCTTCCCTTCTTGAGTCCAGCTGGTGCCTGGCCAGGGGCTGGGGAGGTG 2870  
GCTGAAGGGTGGGAGAGGCCAGAGGGAGGTCCGGGAGGAGGTCTGGGGAGGAGGTCCAGGGAGGAGGAGG 2940  
AAAGTTCTCAAGTTCGTCTGACATTCAATTCCTGTTAGCACATATTTATCTGAGCACCTACTCTGTGCAGAC 3010  
GCTGGGCTAAGTGCTGGGGACACAGCAGGGGAACAAGGCAGACATGGAATCTGCACTCGAG 3070

FIG. 3E

10 / 16

## FIG. 4

### EChpG-CSFDNA SECTION I

10 1 20 30 40 50 60  
CTAGAAAA ACCAAGGAGG TAATAAATAA TGACTCCATT AGTCCCTGCT TCTTCTCTGC  
TTTTT TGGTTCCTCC ATTATTTATT ACTGAGGTAA TCCAGGACCGA AGAAGAGACG  
8 9

XbaI

70 3 80 90 100 110 120  
CGCAAAGCTT TCTGCTGAAA TGTCGTGAAC AGGTTCGTAA AATCCAGGGT GACGGTGCTG  
GCGTTTCGAA AGACGACTTT ACAGACCTTG TCCAAGCATT TTAGGTCCCA CTGCCACGAC  
10 11

130 5 140 150 160 170 180  
CACTGCAAGA AAAACTGTGC GCTACTTACA AACTGTGCCA TCCGGAAGAG CTGGTACTGC  
GTGACGTCT TTTTGACACG CGATGAATGT TTGACACGGT AGGCTTCTG GACCATGACG  
12 13

7 190 100  
TGGGTCATTCTCTTGG  
ACCCAGTAAG AGAACCCCTAG  
14

BamHI

// / 16

## FIG. 5

## EChpG-CSFDNA SECTION II

10 15 20 30 40 50 60  
 GATCCCGTG GGCCTCCGCTG TCTTCTTGTC CATCTCAAGC TCTTCAGCTG GCTGGTTGTC  
 GGCAC CCGAGGCGAC AGAAGAACAG GTAGAGTTCG AGAAGTCGAC CGACCAACAG  
 23 24

BamHI

70 17 80 90 110 120  
 TGTCCTCAACT GCATTCTGGT CTGTTCCTGT ATCAGGGTCT TCTGCAAGCT CTGGAAGGTA  
 ACAGAGTTGA CGTAAGACCA GACAAGGACA TAGTCCCAGA AGACGTTCTGA GACCTTCCAT  
 25 26 27

130 140 150 160 170 180  
 TCTCTCCGGA ACTGGGTCCG ACTCTGGACA CTCTGCAGCT AGATGTAGCT GACTTTGCTA  
 AGAGAGGCCT TGACCCAGGC TGAGACCTGT GAGACGTCGA TCTACATCGA CTGAAACGAT  
 28 29

190 200 210  
 CTACTATTG GCAACAGATG GAAGAGCTCA AAG  
 GATGATAAAC CGTTGTCTAC CTTCTCGAGT TTCTTAA  
 30 SstI EcoRI

12 / 16

## FIG. 6

## EchpG-CSFDNA SECTION III

10 31 20 30 40 50 60  
GATCCAAAG AGCTCGGTAT GGCACCAGCT CTGCAACCGA CTCGAAGGTGC TATGCCGGCA  
GTTTC TCGAGCCATA CCGTGGTCCA GACGTTGGCT GAGTTCCACG ATACGGCCGT  
37 38  
BamHI SstI  
70 33 80 90 100 34 110 120  
TTCGCTTCTG CATTCACGCG TCGTGCAGGA GGTGTACTGG TTGCTTCTCA TCTGCAATCT  
AAGCGAAGAC GTAAGGTCGC AGCACGTCCT CCACATGACC AACGAAGAGT AGACGTTAGA  
39 40  
35 130 140 150 36 160 170  
TTCCTGGAAG TATCTTACCG TGTCTCGCGT CATCTGGCTC AGCCGTAATA G  
AAGGACCTTC ATAGAAATGGC ACAAGACGCA GTAGACCGAG TCGGCATTAT CTTAA  
41 42  
EcoRI

13 / 16

**FIG. 7A**

[illegible]

**FIG. 7B**

[illegible]

## FIG. 8

1 ATCGATTGATTCTAGAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGGTACCAT  
TAGCTAAACTAAGATCTTCCTCCTTATTGTATACCAATTGCGCAACCTTAAGCCATGGTA  
1 Clal, 12 XbaI, 29 NdeI, 35 HincII, HpaI, 39 MluI, 47 EcoRI,  
53 HgiC1 KpnI, 57 NcoI StyI,  
61 GGAAGCTTACTCGAGGATCCGCGGATAAATAAGTAACGATCC  
CCTTCGAATGAGCTCCTAGGCGCCTATTATTCATTGCTAGG  
63 HindIII, 70 AvaI XhoI, 75 BamHI Xho2, 79 Sac2,

16 / 16

<u>Competitor</u>	<u>(U/ml)</u>	<u>WEHI-3B (D<sup>+</sup>)</u>		<u>ANLL (M4)</u>		<u>ANLL (M5B)</u>	
		<u>cpm</u>	<u>% Inhib.</u>	<u>cpm</u>	<u>% Inhib.</u>	<u>cpm</u>	<u>% Inhib.</u>
<u>Exp. 1</u>							
none	0	6,608	-	1,218	-	122	-
natural							
hpG-CSF:	10,000	685	90				
	2,000	1,692	74	34	97	-376	0
	200	2,031	69				
rhG-CSF:	10,000	0	100				
	2,000	1,185	82	202	83	0	0
	200	2,330	65				
<u>Exp. 2</u>							
none	0	2,910	0				
natural							
hpG-CSF:	2,000	628	78				
GM-CSF:	2,000	3,311	0				

FIG. 9